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Query= [gi|10177650|dbj|BAB11112.1](#) cell cycle switch protein
[Arabidopsis thaliana]
(472 letters)

Database: oasis_sap.v1.58

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Query: gi|10177650 (NM_121387) fizzy-related (FZR), putative; protein id: At5g13840.1 [Arabidopsis thaliana]
 Matching gi: 15240729

























































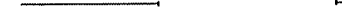





Best hits	Common Tree	Taxonomy Report	3D structures	CDD-Search	GI list
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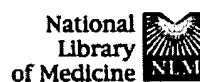
178 BLAST hits to 29 unique species Sort by taxonomy proximity

6 Archaea 54 Bacteria 62 Metazoa 30 Fungi 20 Plants 0 Viruses 6 Other Eukaryotae

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472 aa	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
	2462	19	AAM20433	20466231	cell cycle switch protein [Arabidops:
	1445	19	CAA19806	3292816	putative fizzy-related protein [Arab:
	1445	19	AAM20437	20466239	putative fizzy-related protein [Arab:
	1436	19	AAL36231	17380838	putative Srw1 protein [Arabidopsis th
	1434	14	AAD22612	4558462	cell cycle switch protein [Medicago s
	1434	14	AAF37386	7158292	WD-repeat cell cycle regulatory prote
	1415	19	CAB44330	5002527	Srw1-like protein [Arabidopsis thalia
	1407	11	BAB63690	15289995	putative cell cycle switch protein [C
	1399	19	NP_194022	22328875	fizzy-related (FZR), putative; prote:
	1192	3	CAA74576	2326943	fizzy-related protein [Xenopus laevis
	1183	3	AAC62835	3702286	R33374_1 [Homo sapiens]
	1183	3	BAA86556	6330805	KIAA1242 protein [Homo sapiens]
	1181	3	BAA86954	6463679	Fzr1 [Homo sapiens]
	1181	3	AAD52029	5813825	fizzy-related protein [Mus musculus]
	1167	3	AAF20266	6642733	fizzy-related protein homolog [Homo s
	1164	3	AAF45973	7290520	fzr gene product [Drosophila melanoga
	1164	3	CAA74575	2326419	fizzy-related protein [Drosophila mel
	1134	3	EAA00976	21288683	agCP12792 [Anopheles gambiae str. PE
	1080	3	AAL31949	16930527	CDH1-C [Gallus gallus]
	1060	3	CAA87433	3881613	contains similarity to Pfam domain: 1
	1034	3	AAL31947	16930523	CDH1-A [Gallus gallus]
	999	3	BAA22152	2381494	Srw1 [Schizosaccharomyces pombe]
	983	3	CAA22522	4049501	WD domain; G beta repeat protein [Sch
	922	3	AAF47111	7291689	CG16783-PA [Drosophila melanogaster]
	918	17	CAA11819	3668118	hypothetical protein [Brassica napus]
	912	19	CAB38785	4490294	WD-repeat protein-like protein [Arab:
	912	19	AAF14048	6491862	putative cdc20 protein [Arabidopsis t
	902	19	CAB38784	4490293	WD-repeat protein-like protein [Arab:
	901	3	AAL28117	16755857	CDC20-like 1b [Homo sapiens]
	900	3	BAA86955	6463685	Fzr2 [Homo sapiens]
	892	19	NP_198109	15240985	fizzy-related (FZR), putative; prote:
	885	3	EAA05793	21293648	agCP10238 [Anopheles gambiae str. PE
	882	3	AAC06232	2981095	Cdc20 [Spisula solidissima]
	878	3	AAA83150	1109772	Method: conceptual translation suppl:
	868	19	NP_198060	15240441	fizzy-related (FZR), putative; prote:
	868	19	AAD48933	5732032	contains similarity to Pfam family P1
	867	19	AAB61049	2191163	contains similarity to beta transduc:
	867	19	NP_198042	15240403	fizzy-related (FZR), putative; prote:
	866	3	AAC41376	3298595	fizzyl [Xenopus laevis]
	863	3	AAC14741	3088632	cell cycle protein p55CDC [Rattus nor
	861	3	AAH03215	13096838	Similar to cell cycle protein p55CDC
	860	3	AAA19017	468032	p55CDC [Homo sapiens]

	860	3	AAH00624	12653679	CDC20 (cell division cycle 20, S. ce
	860	3	BAA97451	8885513	Cdc20 [Mus musculus]
	860	3	AAD16405	4323528	cell cycle protein CDC20 [Homo sapien
	859	3	AAA19018	468034	p55CDC [Rattus norvegicus]
	854	3	BAB27422	12847059	cell division cycle 20 homolog (S. ce
	850	13	AAB63030	2253631	WD-repeat protein [Daucus carota]
	833	3	CAA96703	1322451	ORF YGL003c [Saccharomyces cerevisiae]
	793	3	AAC49621	1794292	WD-domain protein [Schizosaccharomyc
	758	19	NP_568505	18421178	fizzy-related (FZR), putative; prote
	744	3	CAB98424	15426166	probable hypothetical 13.7 Kd protein
	692	3	AAK29632	13549094	p55CDC [Sus scrofa]
	689	3	AAD26623	4633085	fizzy-related protein [Homo sapiens]
	661	3	P26309	461700	Cell division control protein 20
	661	3	BAA03957	416288	ORF1 [Saccharomyces cerevisiae]
	632	3	CAD25313	19068845	CDC20-LIKE PROTEIN [Encephalitozoon
	573	3	BAC04508	21754461	unnamed protein product [Homo sapien
	565	3	AAL31948	16930525	CDH1-B [Gallus gallus]
	560	3	CAA42058	3645	Cdc20 [Saccharomyces cerevisiae]
	517	3	AAB51112	1915987	CDC20 [Tritrichomonas foetus]
	484	3	CAD26295	19168776	similarity to CDC20 (WD-repeat prote
	457	3	XP_138861	20898546	similar to fizzy1 [Mus musculus]
	400	3	CAA91101	1008993	putative cdc protein; WD repeat [Sch
	393	3	NP_011741	6681847	Required for sporulation, highly indu
	392	3	AAK61800	14486175	Amalp [Saccharomyces cerevisiae]
	389	3	CAA22488	4008571	putative WD-domain protein [Schizosa
	358	3	XP_139652	20896939	similar to cell division cycle 20 hor
	350	3	AAL31950	16930529	CDH1-D [Gallus gallus]
	333	3	AAG00051	9803044	Hypothetical protein ZK177.6 [Caenorl
	287	3	T27762	7511009	hypothetical protein ZK177.6 - Caeno
	284	3	CAD01127	16416039	related to fzf protein [Neurospora c
	281	3	XP_142169	20985567	similar to cell cycle protein p55CDC
	277	2	BAB75165	17132599	WD-40 repeat protein [Nostoc sp. PCC
	257	2	BAB76258	17133695	WD-40 repeat-protein [Nostoc sp. PCC
	248	2	BAB72396	17129783	serine/threonine kinase with WD-40 re
	248	3	BAB97393	21322756	G6VTS76519 minor form-1 [Homo sapien
	248	3	XP_094210	22050291	similar to G6VTS76519 minor form-1 [H
	247	3	AAK29631	13549092	fizzy-related protein FZR [Sus scrofa
	244	2	BAB74499	17131893	WD-repeat protein [Nostoc sp. PCC 71
	291	2	BAB77807	17135261	WD-40 repeat protein [Nostoc sp. PCC
	226	2	BAB78213	17135667	WD-repeat protein [Nostoc sp. PCC 71
	224	3	AAD35017	4973280	Ebi [Drosophila melanogaster]
	247	2	BAB77771	17135225	WD-40 repeat protein [Nostoc sp. PCC
	223	2	BAB76458	17133896	WD-repeat protein [Nostoc sp. PCC 71
	222	3	AAB81475	9931971	general transcriptional repressor Tup
	222	3	CAB52736	5734475	general transcriptional repressor tup
	219	3	CAC81004	18076173	transcriptional repressor, TUP1 [Yar
	252	2	BAB74818	17132214	ORF_ID:alr3119-WD repeat protein with
	210	2	BAC08041	22294210	WD-40 repeat protein [Thermosynechoc
	207	2	AAM05961	19916545	WD-domain containing protein [Methano
	222	3	AAL37301	17225210	beta transducin-like protein HET-D2Y
	202	3	AAC29438	3406654	transcriptional repressor TUP1 [Dicty
	202	3	AAG28504	11066216	TUPA [Emericella nidulans]
	212	2	BAB72622	17130010	WD-40 repeat protein [Nostoc sp. PCC
	201	3	T49342	11289987	fzf related protein [imported] - Neu
	200	3	AAK93119	15291701	LD24014p [Drosophila melanogaster]
	200	3	AAF51974	7296695	CG1109 gene product [Drosophila melar
	237	2	BAB77808	17135262	WD-40 repeat protein [Nostoc sp. PCC
	197	3	AAB37245	1698504	rco-1 gene product [Neurospora crassa
	197	3	Q17963	3123159	HYPOTHETICAL 40.4 KD TRP-ASP REPEATS
	195	3	AAH01353	12655011	katanin p80 (WD40-containing) subunit
	195	3	BAB26884	12845754	data source:SPTR, source key:060620,
	195	3	XP_134311	20885985	katanin p80 (WD40-containing) subunit



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Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned P1 clones.

PubMed
Services**Sato S, Kotani H, Nakamura Y, Kaneko T, Asamizu E, Fukami M, Miyajima N, Tabata S.**

Kazusa DNA Research Institute, Chiba, Japan.

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Resources

A total of 20 P1 clones with an average insert size of 80 kb and each containing a marker(s) specifically mapped on chromosome 5 were isolated from a P1 library of the Arabidopsis thaliana genome, and their nucleotide sequences were determined according to a shotgun-based strategy and precisely located on the physical map of chromosome 5 separately constructed. The total length of the sequenced regions were summed up to 1,621,245 bp. By comparison with the sequences in protein and EST databases and analysis with computer programs for gene modeling, a total of 347 potential protein-coding genes and/or gene segments with known or predicted functions were identified. The positions of exons which do not exhibit any similarity to known genes were also predicted. An average density of the genes and/or gene segments assigned so far as 1 gene/4,672 bp. Introns were identified in approximately 78% of the potential genes, and the average number and length of the introns per gene were 3.7 and 161 bp. The transcription level of the predicted genes was roughly monitored by counting the numbers of identified Arabidopsis ESTs. The sequence data and gene information are available through the World Wide Web at <http://www.kazusa.or.jp/arabi/>.

MeSH Terms:

- Arabidopsis/genetics*
- Chromosome Mapping*
- DNA, Plant/analysis*
- Genetic Markers/genetics
- Genomic Library*
- Open Reading Frames*
- Sequence Analysis, DNA
- Support, Non-U.S. Gov't

Substances:

- Genetic Markers

- DNA, Plant

Secondary source id:

- GENBANK/AB005249
- GENBANK/AB005248
- GENBANK/AB005247
- GENBANK/AB005246
- GENBANK/AB005245
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- GENBANK/AB005234
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- GENBANK/AB005232
- GENBANK/AB005231
- GENBANK/AB005230

PMID: 9330910 [PubMed - indexed for MEDLINE]

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